APPLICATION NO./ CONTROL NO.	FILING DATE	FIRST NAMED INVENTOR / PATENT IN REEXAMINATION	ATTORNEY DOCKET NO.

EXAMINER Sarada Prasad

ART UNIT	PAPER
1646	8

DATE MAILED:

Please find below and/or attached an Office communication concerning this application or proceeding.

Commissioner of Patents

Sequence Rules

The reply filed on 8/16/01 (Paper No. 7) is not fully responsive to the prior Office Action because of the following omission(s) or matter(s):

See attached Raw sequence listing -error report.

Since the above-mentioned reply appears to be bona fide, applicant is given ONE (1) MONTH or THIRTY (30) DAYS from the mailing date of this notice, whichever is longer, within which to supply the omission or correction in order to avoid abandonment. EXTENSIONS OF THIS TIME PERIOD MAY BE GRANTED UNDER 37 CFR 1.136(a)

Advisory Information

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Sarada C Prasad whose telephone number is 703-305-1009. The examiner can normally be reached Monday – Friday from 8.00 AM to 4.30 PM (Eastern time).

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Yvonne Eyler, can be reached on (703) 308-6564. The fax phone number for the organization where this application or proceeding is assigned is 703-308-0294.

Any inquiry of a general nature or relating to the status of this application or proceeding should be directed to the receptionist whose telephone number is 703-308-0196.

Sarada Prasad, Ph.D.
Examiner
Art Unit 1646
September 10, 2001

PREMA MERTZ
PRIMARY EXAMINER

PTO-90C (Rev.3-98)

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: *09/508,570*

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1_____Wrapped Nucleics
     Wrapped Aminos

The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

·2_____Invalid Line Length

The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 ✓ Misaligned Amino
     Numbering

The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4_____Non-ASCII

The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5_____Variable Length·

Sequence(s)_____contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6_____PatentIn 2.0
     "bug"

A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7_____Skipped Sequences
     (OLD RULES)

Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8_____Skipped Sequences
     (NEW RULES)

Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9_____Use of n's or Xaa's
     (NEW RULES)

Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10_____Invalid <213>
     Response

Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11_____Use of <220>

Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of Sequence Rules)

12_____·PatentIn 2.0
     "bug"·

Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13_____Misuse of n

n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

1600

```
            RAW SEQUENCE LISTING          DATE: 09/06/2001
            PATENT APPLICATION:  US/09/508,510   TIME: 17:52:33

            Input Set : A:\56400002-sequence.txt
            Output Set: N:\CRF3\09062001\I508510.raw
```

pp 1-3

Does Not Comply
Corrected Diskette Needed

```
     3 <110> APPLICANT: Tschope, Michael;
     4        Siklosi, Thomas;
     5        Schroeder, Peter; and
     6        Hofer, Hans.
     8 <120> TITLE OF INVENTION: Liquid Interferon-BETA Formulations
    10 <130> FILE REFERENCE: 17150P US WO (DR)
C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/508,510
    13 <141> CURRENT FILING DATE: 2000-05-26
    15 <150> PRIOR APPLICATION NUMBER: PCT/EP98/06065 and EP 97 116 562.6
W--> 16 <151> PRIOR FILING DATE: 1998-09-23 (PCT/EP98/06065) and 1997-09-23 (EP 97 116 562.6)
    18 <160> NUMBER OF SEQ ID NOS: 14
    20 <170> SOFTWARE: PatentIn Ver. 2.1
```

list these or separate <150> and <151>

ERRORED SEQUENCES

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    22 <210> SEQ ID NO: 1
    23 <211> LENGTH: 7
    24 <212> TYPE: PRT
    25 <213> ORGANISM: Homo sapiens
    27 <400> SEQUENCE: 1
    28 Glu Asp Phe Thr Arg Gly Lys
E--> 29  1           5        5
    33 <210> SEQ ID NO: 2
    34 <211> LENGTH: 6
    35 <212> TYPE: PRT
    36 <213> ORGANISM: Homo sapiens
    38 <400> SEQUENCE: 2
    39 Thr Val Leu Glu Glu Lys
E--> 40  1              5
    44 <210> SEQ ID NO: 3
    45 <211> LENGTH: 7
    46 <212> TYPE: PRT
    47 <213> ORGANISM: Homo sapiens
    49 <400> SEQUENCE: 3
    50 Gln Leu Gln Gln Phe Gln Lys
E--> 51  1                  5
    55 <210> SEQ ID NO: 4
    56 <211> LENGTH: 8
    57 <212> TYPE: PRT
    58 <213> ORGANISM: Homo sapiens
    60 <400> SEQUENCE: 4
E--> 61 Leu Xaa Ser Ser Leu His Leu Lys
E--> 62  1                  5
    66 <210> SEQ ID NO: 5
    67 <211> LENGTH: 8
    68 <212> TYPE: PRT
```

misaligned amino acid number (global error) see item 3 on Error Summary Sheet

same error

see item 9 on Error Summary Sheet

RAW SEQUENCE LISTING   DATE: 09/06/2001
PATENT APPLICATION: US/09/508,510   TIME: 17:52:33

Input Set : A:\56400002-sequence.txt
Output Set: N:\CRF3\09062001\I508510.raw


```
     69 <213> ORGANISM: Homo sapiens
     71 <400> SEQUENCE: 5
     72 Leu Met Ser Ser Leu His Leu Lys
E--> 73    1                         5
     75 <210> SEQ ID NO: 6
     76 <211> LENGTH: 12
     77 <212> TYPE: PRT
     78 <213> ORGANISM: Homo sapiens      item 9
     80 <400> SEQUENCE: 6
E--> 81 Asp Arg Xaa Asn Phe Asp Ile Pro Glu Glu Ile Lys
E--> 82    1                         5                    10
     86 <210> SEQ ID NO: 7
     87 <211> LENGTH: 11
     88 <212> TYPE: PRT
     89 <213> ORGANISM: Homo sapiens
     91 <400> SEQUENCE: 7
     92 Arg Tyr Tyr Gly Arg Ile Leu His Tyr Leu Lys
E--> 93    1                         5                    10
     97 <210> SEQ ID NO: 8
     98 <211> LENGTH: 12
     99 <212> TYPE: PRT
    100 <213> ORGANISM: Homo sapiens
    102 <400> SEQUENCE: 8
    103 Asp Arg Met Asn Phe Asp Ile Pro Glu Glu Ile Lys
E--> 104   1                         5                    10
    108 <210> SEQ ID NO: 9
    109 <211> LENGTH: 14
    110 <212> TYPE: PRT
    111 <213> ORGANISM: Homo sapiens
E--> 112 <400> SEQUENCE: 9
    113 Leu Leu Trp Gln Leu Asn Gly Arg Leu Glu Tyr Cys Leu Lys
E--> 114   1                         5                    10
    118 <210> SEQ ID NO: 10
    119 <211> LENGTH: 19
    120 <212> TYPE: PRT
    121 <213> ORGANISM: Homo sapiens
    123 <400> SEQUENCE: 10                  item 9
E--> 124 Xaa Ser Tyr Asn Leu Leu Gly Phe Leu Gln Arg Ser Ser Asn Phe Gln
E--> 125
       1                   5                   10                   15
    127 Cys Gln Lys
    132 <210> SEQ ID NO: 11
    133 <211> LENGTH: 19
    134 <212> TYPE: PRT
    135 <213> ORGANISM: Homo sapiens
    137 <400> SEQUENCE: 11
    138 Met Ser Tyr Asn Leu Leu Gly Phe Leu Gln Arg Ser Ser Asn Phe Gln
E--> 139
       1                   5                   10                   15
    141 Cys Gln Lys
    146 <210> SEQ ID NO: 12
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      147 <211> LENGTH: 30
      148 <212> TYPE: PRT
      149 <213> ORGANISM: Homo sapiens
      151 <400> SEQUENCE: 12
      152 Glu Tyr Ser His Cys Ala Trp Thr Ile Val Arg Val Glu Ile Leu Arg
E--> 153    1              5           10                    15
      155 Asn Phe Tyr Phe Ile Asn Arg Leu Thr Gly Tyr Leu Arg Asn
E--> 156              20           25                    30
      160 <210> SEQ ID NO: 13
      161 <211> LENGTH: 47
      162 <212> TYPE: PRT
      163 <213> ORGANISM: Homo sapiens
      165 <400> SEQUENCE: 13
E--> 166 Glu Asp Ala Ala Leu Thr Ile Tyr Glu Xaa Leu Gln Asn Ile Phe Ala
E--> 167
        1              5           10                    15
      169 Ile Phe Arg Gln Asp Ser Ser Ser Thr Gly Trp Asn Glu Thr Ile Val
E--> 170              20           25                    30
      172 Glu Asn Leu Leu Ala Asn Val Tyr His Gln Ile Asn His Leu Lys
E--> 173              35           40           45
      177 <210> SEQ ID NO: 14
      178 <211> LENGTH: 47
      179 <212> TYPE: PRT
      180 <213> ORGANISM: Homo sapiens
      182 <400> SEQUENCE: 14
      183 Glu Asp Ala Ala Leu Thr Ile Tyr Glu Met Leu Gln Asn Ile Phe Ala
E--> 184
        1              5           10                    15
      186 Ile Phe Arg Gln Asp Ser Ser Ser Thr Gly Trp Asn Glu Thr Ile Val
E--> 187              20           25                    30
      189 Glu Asn Leu Leu Ala Asn Val Tyr His Gln Ile Asn His Leu Lys
E--> 190              35           40           45
E--> 194 VI
      196 I
E--> 198 VI
      200 I
E--> 202 IV
E--> 204 I
```

item 9

delete at end of file

VERIFICATION SUMMARY
PATENT APPLICATION: **US/09/508,510**

DATE: 09/06/2001
TIME: 17:52:34

Input Set : **A:\56400002-sequence.txt**
Output Set: **N:\CRF3\09062001\I508510.raw**

```
L:12 M:270 C: Current Application Number differs, Replaced Current Application Number
L:16 M:256 W: Invalid Numeric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD
L:29 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:1
L:40 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:2
L:51 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:3
L:61 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:4
M:332 Repeated in SeqNo=4
L:73 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:5
L:81 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:6
M:332 Repeated in SeqNo=6
L:93 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:7
L:104 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:8
L:112 M:283 W: Missing Blank Line separator, <400> field identifier
L:114 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:9
L:124 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:10
M:332 Repeated in SeqNo=10
L:139 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:11
L:153 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:12
M:332 Repeated in SeqNo=12
L:166 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:13
M:332 Repeated in SeqNo=13
L:184 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:14
M:332 Repeated in SeqNo=14
L:194 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:194 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:198 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:198 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:202 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:202 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:204 M:252 E: No. of Seq. differs, <211>LENGTH:Input:47 Found:50 SEQ:14
```